



PCT

RAW SEQUENCE LISTING

DATE: 07/06/2004

PATENT APPLICATION: US/10/500,216

TIME: 12:19:14

Input Set : A:\61534 Sequence Listing.txt

Output Set: N:\CRF4\07062004\J500216.raw

5 <110> APPLICANT: Takeda Chemical Industries, Ltd.
 7 <120> TITLE OF INVENTION: Preventives/Remedies For Cancer
 9 <130> FILE REFERENCE: P02-0148PCT
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/500,216
 C--> 11 <141> CURRENT FILING DATE: 2004-06-24
 11 <150> PRIOR APPLICATION NUMBER: JP2001-398220
 12 <151> PRIOR FILING DATE: 2001-12-27
 14 <160> NUMBER OF SEQ ID NOS: 19
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 412
 18 <212> TYPE: PRT
 19 <213> ORGANISM: Human
 21 <400> SEQUENCE: 1

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 22 | Met | Ala | Glu | Asn | Leu | Lys | Gly | Cys | Ser | Val | Cys | Cys | Lys | Ser | Ser | Trp | |
| 23 | | | | | 5 | | | | | 10 | | | | | | 15 | |
| 24 | Asn | Gln | Leu | Gln | Asp | Leu | Cys | Arg | Leu | Ala | Lys | Leu | Ser | Cys | Pro | Ala | |
| 25 | | | | 20 | | | | | 25 | | | | | 30 | | | |
| 26 | Leu | Gly | Ile | Ser | Lys | Arg | Asn | Leu | Tyr | Asp | Phe | Glu | Val | Glu | Tyr | Leu | |
| 27 | | | | 35 | | | | 40 | | | | | 45 | | | | |
| 28 | Cys | Asp | Tyr | Lys | Lys | Ile | Arg | Glu | Gln | Glu | Tyr | Tyr | Leu | Val | Lys | Trp | |
| 29 | | 50 | | | | | 55 | | | | | 60 | | | | | |
| 30 | Arg | Gly | Tyr | Pro | Asp | Ser | Glu | Ser | Thr | Trp | Glu | Pro | Arg | Gln | Asn | Leu | |
| 31 | 65 | | | | | 70 | | | | 75 | | | | | 80 | | |
| 32 | Lys | Cys | Val | Arg | Ile | Leu | Lys | Gln | Phe | His | Lys | Asp | Leu | Glu | Arg | Glu | |
| 33 | | | | 85 | | | | | 90 | | | | | 95 | | | |
| 34 | Leu | Leu | Arg | Arg | His | His | Arg | Ser | Lys | Thr | Pro | Arg | His | Leu | Asp | Pro | |
| 35 | | | | 100 | | | | | 105 | | | | | 110 | | | |
| 36 | Ser | Leu | Ala | Asn | Tyr | Leu | Val | Gln | Lys | Ala | Lys | Gln | Arg | Arg | Ala | Leu | |
| 37 | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 38 | Arg | Arg | Trp | Glu | Gln | Glu | Leu | Asn | Ala | Lys | Arg | Ser | His | Leu | Gly | Arg | |
| 39 | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 40 | Ile | Thr | Val | Glu | Asn | Glu | Val | Asp | Leu | Asp | Gly | Pro | Pro | Arg | Ala | Phe | |
| 41 | 145 | | | | | 150 | | | | | 155 | | | | 160 | | |
| 42 | Val | Tyr | Ile | Asn | Glu | Tyr | Arg | Val | Gly | Glu | Gly | Ile | Thr | Leu | Asn | Gln | |
| 43 | | | | 165 | | | | | 170 | | | | | 175 | | | |
| 44 | Val | Ala | Val | Gly | Cys | Glu | Cys | Gln | Asp | Cys | Leu | Trp | Ala | Pro | Thr | Gly | |
| 45 | | | | 180 | | | | 185 | | | | | 190 | | | | |
| 46 | Gly | Cys | Cys | Pro | Gly | Ala | Ser | Leu | His | Lys | Phe | Ala | Tyr | Asn | Asp | Gln | |
| 47 | | 195 | | | | | 200 | | | | | 205 | | | | | |
| 48 | Gly | Gln | Val | Arg | Leu | Arg | Ala | Gly | Leu | Pro | Ile | Tyr | Glu | Cys | Asn | Ser | |
| 49 | | 210 | | | | | 215 | | | | 220 | | | | | | |
| 50 | Arg | Cys | Arg | Cys | Gly | Tyr | Asp | Cys | Pro | Asn | Arg | Val | Val | Gln | Lys | Gly | |
| 51 | 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

ENTERED

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52 Ile Arg Tyr Asp Leu Cys Ile Phe Arg Thr Asp Asp Gly Arg Gly Trp
53           245           250           255
54 Gly Val Arg Thr Leu Glu Lys Ile Arg Lys Asn Ser Phe Val Met Glu
55           260           265           270
56 Tyr Val Gly Glu Ile Ile Thr Ser Glu Glu Ala Glu Arg Arg Gly Gln
57           275           280           285
58 Ile Tyr Asp Arg Gln Gly Ala Thr Tyr Leu Phe Asp Leu Asp Tyr Val
59           290           295           300
60 Glu Asp Val Tyr Thr Val Asp Ala Ala Tyr Tyr Gly Asn Ile Ser His
61 305           310           315           320
62 Phe Val Asn His Ser Cys Asp Pro Asn Leu Gln Val Tyr Asn Val Phe
63           325           330           335
64 Ile Asp Asn Leu Asp Glu Arg Leu Pro Arg Ile Ala Phe Phe Ala Thr
65           340           345           350
66 Arg Thr Ile Arg Ala Gly Glu Glu Leu Thr Phe Asp Tyr Asn Met Gln
67           355           360           365
68 Val Asp Pro Val Asp Met Glu Ser Thr Arg Met Asp Ser Asn Phe Gly
69           370           375           380
70 Leu Ala Gly Leu Pro Gly Ser Pro Lys Lys Arg Val Arg Ile Glu Cys
71 385           390           395           400
72 Lys Cys Gly Thr Glu Ser Cys Arg Lys Tyr Leu Phe
73           405           410
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 1236
77 <212> TYPE: DNA
78 <213> ORGANISM: Human
80 <400> SEQUENCE: 2
81 atggcggaattttaaaggctgcagcgtgtgttgcaagctcttcttggaatcagctgcag60
82 gacctgtgccgctggccaa gctctcctgc cctgcectcg gtatctctaa gaggaacctc120
83 tatgactttg aagtcgagta cctgtgcgat tacaagaaga tccgcgaaca ggaatattac180
84 ctgggtgaaatggcgtggata tccagactca gagagcacct gggagccacg gcagaatctc240
85 aagtgtgtgc gtatcctcaa gcagttccac aaggacttag aaaggaggct gctccggcgg300
86 caccaccggt caaagacccc ccggcacctg gaccaagct tggccaacta cctggtgcag360
87 aaggccaagc agaggcgggc gctccgtcgc tgggagcagg agctcaatgc caagcgcagc420
88 catctgggac gcatcactgt agagaatgag gtggacctgg acggccctcc gcgggccttc480
89 gtgtacatca atgagtaccg tgttggtgag ggcatacccc tcaaccagggt ggctgtgggc540
90 tgcgagtgcc aggactgtct gtggggcacc actggaggct gctgcccggg ggcgtcactg600
91 cacaagtttg cctacaatga ccagggccag gtgcggcttc gagccgggct gcccattctac660
92 gagtgcact cccgctgccg ctgcggctat gactgcccac atcgtgtggt acagaagggt720
93 atccgatatg acctctgcat cttccggacg gatgatgggc gtggctgggg cgtccgcacc780
94 ctggagaaga ttgcgaagaa cagcttcgtc atggagtacg tgggagagat cattacctca840
95 gaggaggcag agcggcgggg ccagatctac gaccgtcagg gcgccaccta cctctttgac900
96 ctggactacg tggaggacgt gtacaccgtg gatgccgcct actatggcaa catctcccac960
97 tttgtcaacc acagttgtga cccaacctg cagggtgtaca acgtcttcat agacaacctt1020
98 gacgagcggc tgccccgcat cgctttcttt gccacaagaa ccatccgggc aggcgaggag1080
99 ctcacctttg attacaacat gcaagtggac cccgtggaca tggagagcac ccgcatggac1140
100 tccaactttg gcttggtgg gctccctggc tcccctaaga agcgggtccg tattgaatgc1200
101 aagtgtggga ctgagtcctg ccgcaaatac ctcttc1236
103 <210> SEQ ID NO: 3

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104 <211> LENGTH: 2754
105 <212> TYPE: DNA
106 <213> ORGANISM: Human
108 <400> SEQUENCE: 3
109 ggcacgagggc gcgaggccgg ctaggccccga atgtcgttag ccgtgggggaa agatggcgga      60
110 aaattttaaaa ggctgcagcg tgtgttgcaa gtcttcttgg aatcagctgc aggacctgtg      120
111 ccgcctggcc aagctctcct gccctgccct cggtatctct aagaggaacc tctatgactt      180
112 tgaagtcgag tacctgtgcg attacaagaa gatccgcgaa caggaatatt acctggtgaa      240
113 atggcgtgga tatccagact cagagagcac ctgggagcca cggcagaatc tcaagtgtgt      300
114 gcgtatcctc aagcagttcc acaaggactt agaaaggagg ctgctccggc ggcaccaccg      360
115 gtcaaagacc ccccggcacc tggacccaag ctgggccaac tacctgggtgc agaaggccaa      420
116 gcagaggcgg gcgctccgtc gctgggagca ggagctcaat gccaaagcga gccatctggg      480
117 acgcatcact gtagagaatg aggtggacct ggacggccct ccgcgggcct tcgtgtacat      540
118 caatgagtac cgtgttggtg agggcatcac cctcaaccag gtggctgtgg gctgcgagtg      600
119 ccaggactgt ctgtgggcac ccactggagg ctgctgcccg ggggcgtcac tgcacaagtt      660
120 tgcctacaat gaccagggcc aggtgcggct tcgagccggg ctgcccctct acgagtgcaa      720
121 ctcccgtgc cgctgcggct atgactgccc aaatcgtgtg gtacagaagg gtatccgata      780
122 tgacctctgc atcttccgca cggatgatgg gcgtggctgg ggcgtccgca ccctggagaa      840
123 gattcgcaag aacagcttcg tcatggagta cgtgggagag atcattacct cagaggaggc      900
124 agagcggcgg gccagatct acgaccgtca gggcgccacc tacctctttg acctggacta      960
125 cgtggaggac gtgtacaccg tggatgccgc ctactatggc aacatctccc actttgtcaa      1020
126 ccacagttgt gaccccaacc tgcaggtgta caacgtcttc atagacaacc ttgacgagcg      1080
127 gctgccccgc atcgctttct ttgccacaag aaccatccgg gcaggcgagg agctcacctt      1140
128 tgattacaac atgcaagtgg acccgtgga catggagagc acccgcatgg actccaactt      1200
129 tggcctggct gggctccctg gctcccctaa gaagcgggtc cgtattgaat gcaagtgtgg      1260
130 gactgagtc tgcgcgaaat acctcttcta gcccttagaa gtctgaggcc agactgactg      1320
131 agggggcctg aagctacatg cacctcccc actgctgccc tcctgtcgag aatgactgcc      1380
132 agggcctcgc ctgcctccac ctgccccac ctgctctac ctgctctacg ttcagggtctg      1440
133 tggccgtggt gaggaccgac tccaggagtc cctttccct gtcccagccc catctgtggg      1500
134 ttgcaacttac aaacccccac ccaccttcag aaatagtttt tcaacatcaa gactctctgt      1560
135 cgttgggatt catggcctat taaggaggtc caagggtgta gtcccaaccc agcccagaa      1620
136 tatatttgtt tttgcacctg cttctgcctg gagattgagg ggtctgctgc aggcctcctc      1680
137 cctgtgccc caaaggatg gggaaagcaac ccagagcag gcagacatca gaggccagag      1740
138 tgcctagccc gacatgaagc tggttcccca accacagaaa ctttgtacta gtgaaagaaa      1800
139 gggggtccct gggctacggg ctgaggctgg tttctgctcg tgcttacagt gctgggtagt      1860
140 gttggcccta agagctgtag ggtctcttct tcagggtctgc atatctgaga agtggatgcc      1920
141 cacatgccac tggaaaggaa gtgggtgtcc atgggccact gagcagttag aggaaggcag      1980
142 tgcagagctg gccagccctg gaggtaggct gggaccaagc tctgccttca cagtgcagtg      2040
143 aaggtaccta gggctcttgg gagctctgcg gttgctaggg gccctgacct ggggtgtcat      2100
144 gaccgctgac accactcaga gctggaacca agatctagat agtccgtaga tagcacttag      2160
145 gacaagaatg tgcattgatg ggggtggtgat gaggtgccag gcactgggta gagcacctgg      2220
146 tccacgtgga ttgtctcagg gaagccttga aaaccacgga ggtggatgcc aggaaaagggc      2280
147 ccatgtggca gaaggcaaaag tacaggccaa gaattggggg tgggggagat ggcttcccca      2340
148 ctatgggatg acgaggcgag agggaagccc ttgctgcctg ccattcccag accccagccc      2400
149 tttgtgctca ccctggttcc actggtctca aaagtacact gcctacaaat gtacaaaagg      2460
150 cgaaggttct gatggctgcc ttgctccttg ctccccacc ccctgtgagg acttctctag      2520
151 gaagtccttc ctgactacct gtgccagag tgcccctaca tgagactgta tgccctgcta      2580
152 tcagatgcca gatctatgtg tctgtctgtg tgtccatccc gccgaccccc cagactaacc      2640
153 tccaggcatg gactgaatct ggttctcctc ttgtacaccc ctcaacccta tgcagcctgg      2700

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```

154 agtgggcatc aataaaatga actgtcgact gaaaaaaaaa aaaaaaaaaa aaaa      2754
156 <210> SEQ ID NO: 4
157 <211> LENGTH: 20
158 <212> TYPE: DNA
159 <213> ORGANISM: Artificial Sequence
161 <220> FEATURE:
162 <223> OTHER INFORMATION: Primer
164 <400> SEQUENCE: 4
165 atgcgtccca gatggctgcg      20
167 <210> SEQ ID NO: 5
168 <211> LENGTH: 20
169 <212> TYPE: DNA
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Primer
175 <400> SEQUENCE: 5
176 gcgtcggtag accctgcgta      20
178 <210> SEQ ID NO: 6
179 <211> LENGTH: 18
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <223> OTHER INFORMATION: Primer
186 <400> SEQUENCE: 6
187 aaccttgacg agcggctg      18
189 <210> SEQ ID NO: 7
190 <211> LENGTH: 14
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Primer
197 <400> SEQUENCE: 7
198 tcgcctgccg gatg      14
200 <210> SEQ ID NO: 8
201 <211> LENGTH: 23
202 <212> TYPE: DNA
203 <213> ORGANISM: Artificial Sequence
205 <220> FEATURE:
206 <223> OTHER INFORMATION: Probe
208 <400> SEQUENCE: 8
209 ccgcatcgct ttctttgccca caa      23
211 <210> SEQ ID NO: 9
212 <211> LENGTH: 24
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Primer
219 <400> SEQUENCE: 9
220 ggaaagatgg cggaaaattt aaaa      24

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```

222 <210> SEQ ID NO: 10
223 <211> LENGTH: 24
224 <212> TYPE: DNA
225 <213> ORGANISM: Artificial Sequence
227 <220> FEATURE:
228 <223> OTHER INFORMATION: Primer
230 <400> SEQUENCE: 10
231 gggctagaag aggtatttgc ggca 24
233 <210> SEQ ID NO: 11
234 <211> LENGTH: 31
235 <212> TYPE: DNA
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Primer
241 <400> SEQUENCE: 11
242 ccggaattcg cggaaaattt aaaaggctgc a 31
244 <210> SEQ ID NO: 12
245 <211> LENGTH: 29
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Primer
252 <400> SEQUENCE: 12
253 ccgctcgagc tagaagaggt atttgcggc 29
255 <210> SEQ ID NO: 13
256 <211> LENGTH: 32
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Primer
263 <400> SEQUENCE: 13
264 ccgctcgagc tagccacag ccacctggtt ga 32
266 <210> SEQ ID NO: 14
267 <211> LENGTH: 113
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Primer
274 <400> SEQUENCE: 14
275 ggggtaccaa gatggagcag aaactcatct ctgaagagga tctggagcag aaactcatct 60
276 ctgaagagga tctggagcag aaactcatct ctgaagagga tctggaattc cgg 113
278 <210> SEQ ID NO: 15
279 <211> LENGTH: 113
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Primer
286 <400> SEQUENCE: 15
287 ccggaattcc agatcctctt cagagatgag tttctgctcc agatcctctt cagagatgag 60

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date